Package: babette (via r-universe)

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Title Control 'BEAST2'

Version 2.3.4

Description 'BEAST2' (<https://www.beast2.org>) is a widely used Bayesian phylogenetic tool, that uses DNA/RNA/protein data and many model priors to create a posterior of jointly estimated phylogenies and parameters. 'BEAST2' is commonly accompanied by 'BEAUti 2', 'Tracer' and 'DensiTree'. 'babette' provides for an alternative workflow of using all these tools separately. This allows doing complex Bayesian phylogenetics easily and reproducibly from 'R'.

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RoxygenNote 7.2.3

VignetteBuilder knitr

URL https://docs.ropensci.org/babette/ (website), https://github.com/ropensci/babette

BugReports https://github.com/ropensci/babette/issues

Depends beautier (>= 2.6.12), beastier (>= 2.5), mauricer (>= 2.5.2), R (>= 3.5.0), tracerer

Imports phangorn, rlang (>= 1.1.0), stringr, xml2

Suggests ape, ggplot2, knitr, lintr, nLTT, rappdirs, rmarkdown, spelling, testthat (>= 2.1.0)

Language en-US

Encoding UTF-8

SystemRequirements BEAST2 (https://www.beast2.org/)

Repository https://ropensci.r-universe.dev

RemoteUrl https://github.com/ropensci/babette

RemoteRef master

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Contents

`bbt_continue` *Continue a BEAST2 run*

Description

Do a full run: create a 'BEAST2' configuration file (like 'BEAUti 2'), run 'BEAST2', parse results (like 'Tracer')

Usage

```
bbt_continue(fasta_filename, inference_model, beast2_options)
```

Arguments

`fasta_filename`	a FASTA filename
`inference_model`	a Bayesian phylogenetic inference model, as returned by create_inference_model
`beast2_options`	'BEAST2' options, as can be created by create_beast2_options

Value

a list with the following elements:

- `estimates`: a data frame with 'BEAST2' parameter estimates

- `[alignment_id]_trees`: a `multiPhylo` containing the phylogenies in the 'BEAST2' posterior. `[alignment_id]` is the ID of the alignment. For example, when running `bbt_run_from_model` with `anthus_aco.fas`, this element will have name `anthus_aco_trees`
- `operators`: a data frame with the 'BEAST2' MCMC operator acceptances
- `output`: a numeric vector with the output sent to standard output and error streams
- `ns`: (optional) the results of a marginal likelihood estimation, will exist only when `create_ns_mcmc` was used for `mcmc`. This structure will contain the following elements:
  - `marg_log_lik` the marginal log likelihood estimate
  - `marg_log_lik_sd` the standard deviation around the estimate
  - `estimates` the parameter estimates created during the marginal likelihood estimation
  - `trees` the trees created during the marginal likelihood estimation

Author(s)

Richèl J.C. Bilderbeek

See Also

Use `remove_burn_ins` to remove the burn-ins from the posterior's estimates (`posterior$estimates`)

Examples

```
if (beautier::is_on_ci() && is_beast2_installed()) {
  beastier::remove_beaustier_folders()
  beastier::check_empty_beaustier_folders()

  # A simple FASTA file
  fasta_filename <- beautier::get_beautier_path("test_output_0.fas")

  # Simple short inference
  inference_model <- create_test_inference_model()

  # Default BEAST2 options
  beast2_options <- create_beast2_options()

  bbt_run_from_model(
    fasta_filename = fasta_filename,
    inference_model = inference_model,
    beast2_options = beast2_options
  )

  bbt_continue(
    fasta_filename = fasta_filename,
    inference_model = inference_model,
    beast2_options = beast2_options
  )

  # Cleanup
  bbt_delete_temp_files(
    inference_model = inference_model,
```

```
  beast2_options = beast2_options
)
beastier::remove_beaustier_folders()
beastier::check_empty_beaustier_folders()
}
```

`bbt_delete_temp_files` *Delete all the temporary files created by bbt_run_from_model*

Description

Delete all the temporary files created by bbt_run_from_model

Usage

```
bbt_delete_temp_files(inference_model, beast2_options)
```

Arguments

`inference_model`	a Bayesian phylogenetic inference model, as returned by create_inference_model
`beast2_options`	'BEAST2' options, as can be created by create_beast2_options

Value

Nothing.

Author(s)

Richèl J.C. Bilderbeek

Examples

```
if (beautier::is_on_ci() && is_beast2_installed()) {
  beastier::remove_beaustier_folders()
  beastier::check_empty_beaustier_folders()

  # Do a minimal run
  inference_model <- create_test_inference_model()
  beast2_options <- create_beast2_options()
  bbt_run_from_model(
    fasta_filename = get_fasta_filename(),
    inference_model = inference_model,
    beast2_options = beast2_options
  )

  # Cleanup
  bbt_delete_temp_files(
    inference_model = inference_model,
```

```
    beast2_options = beast2_options
  )

  beastier::remove_beaustier_folders()
  beastier::check_empty_beaustier_folders()
}
```

---

bbt_run *Run BEAST2*

Description

Do a full BEAST2 run: create a 'BEAST2' configuration file (like 'BEAUti 2'), run 'BEAST2', parse results (like 'Tracer')

Usage

```
bbt_run(
  fasta_filename,
  tipdates_filename = NA,
  site_model = beautier::create_jc69_site_model(),
  clock_model = beautier::create_strict_clock_model(),
  tree_prior = beautier::create_yule_tree_prior(),
  mrca_prior = NA,
  mcmc = beautier::create_mcmc(),
  beast2_input_filename = beastier::create_temp_input_filename(),
  rng_seed = 1,
  beast2_output_state_filename = beastier::create_temp_state_filename(),
  beast2_path = beastier::get_default_beast2_path(),
  overwrite = TRUE,
  verbose = FALSE
)
```

Arguments

fasta_filename	a FASTA filename
tipdates_filename	name of the file containing tip dates
site_model	one site model, see create_site_models
clock_model	one clock model, see create_clock_model
tree_prior	one tree priors, as created by create_tree_prior
mrca_prior	one Most Recent Common Ancestor prior, as returned by create_mrca_prior
mcmc	the MCMC options, see create_mcmc

`beast2_input_filename`
: path of the 'BEAST2' configuration file. By default, this file is put in a temporary folder with a random filename, as the user needs not read it: it is used as input of 'BEAST2'. Specifying a `beast2_input_filename` allows to store that file in a more permanently stored location.

`rng_seed`
: the random number generator seed. Must be either `NA` or a positive non-zero value. An RNG seed of `NA` results in 'BEAST2' picking a random seed.

`beast2_output_state_filename`
: name of the final state file created by 'BEAST2', containing the operator acceptances. By default, this file is put a temporary folder with a random filename, as the user needs not read it: its content is parsed and returned by this function. Specifying a `beast2_output_state_filename` allows to store that file in a more permanently stored location.

`beast2_path`
: name of either a 'BEAST2' binary file (usually simply `beast`) or a 'BEAST2' jar file (usually has a `.jar` extension). Use `get_default_beast2_bin_path` to get the default BEAST binary file's path Use `get_default_beast2_jar_path` to get the default BEAST jar file's path

`overwrite`
: will 'BEAST2' overwrite files? Like 'BEAST2', this is set to TRUE by default. If TRUE, 'BEAST2' will overwrite the `beast2_options$output_state_filename` if its present. If FALSE, 'BEAST2' will not overwrite the `beast2_options$output_state_filename` if its present and babette will give an error message. Note that if `overwrite` is set to FALSE when a `tracelog` (see create_tracelog), `screenlog` (see create_screenlog) or `treelog` (see create_treelog) file already exists, 'BEAST2' (and thus babette) will freeze.

`verbose`
: set to TRUE for more output

Details

Prefer using `bbt_run_from_model`, as it has a cleaner interface.

Value

a list with the following elements:

- `estimates`: a data frame with 'BEAST2' parameter estimates
- `[alignment_id]_trees`: a `multiPhylo` containing the phylogenies in the 'BEAST2' posterior. `[alignment_id]` is the ID of the alignment. For example, when running `bbt_run` with `anthus_aco.fas`, this element will have name `anthus_aco_trees`
- `operators`: a data frame with the 'BEAST2' MCMC operator acceptances
- `output`: a numeric vector with the output sent to standard output and error streams
- `ns`: (optional) the results of a marginal likelihood estimation, will exist only when `create_ns_mcmc` was used for the MCMC. This structure will contain the following elements:
  - `marg_log_lik` the marginal log likelihood estimate
  - `marg_log_lik_sd` the standard deviation around the estimate
  - `estimates` the parameter estimates created during the marginal likelihood estimation
  - `trees` the trees created during the marginal likelihood estimation

Author(s)

Richèl J.C. Bilderbeek

See Also

Use `remove_burn_ins` to remove the burn-ins from the posterior's estimates (`posterior$estimates`)

Examples

```
if (beautier::is_on_ci() && is_beast2_installed()) {
  beastier::remove_beaustier_folders()
  beastier::check_empty_beaustier_folders()

  # Setup for a short run
  mcmc <- create_test_mcmc()

  # Store filenames for cleanup.
  # Note that 'bbt_run_from_model allows for easier cleanup
  mcmc$tracelog$filename <- tempfile()
  mcmc$treelog$filename <- tempfile()
  mcmc$screenlog$filename <- tempfile()
  beast2_input_filename <- tempfile()
  beast2_output_state_filename <- tempfile()

  bbt_run(
    fasta_filename = get_babette_path("anthus_aco.fas"),
    beast2_input_filename = beast2_input_filename,
    beast2_output_state_filename = beast2_output_state_filename,
    mcmc = mcmc
  )

  # Cleanup
  # Again, note that 'bbt_run_from_model allows for easier cleanup
  file.remove(mcmc$tracelog$filename)
  file.remove(mcmc$treelog$filename)
  file.remove(mcmc$screenlog$filename)
  file.remove(beast2_input_filename)
  file.remove(beast2_output_state_filename)
  beastier::remove_beaustier_folders()
  beastier::check_empty_beaustier_folders()
}
```

---

bbt_run_from_model *Run BEAST2*

Description

Do a full run: create a 'BEAST2' configuration file (like 'BEAUti 2'), run 'BEAST2', parse results (like 'Tracer')

Usage

```
bbt_run_from_model(
  fasta_filename,
  inference_model = beautier::create_inference_model(),
  beast2_options = beastier::create_beast2_options()
)
```

Arguments

`fasta_filename`	a FASTA filename
`inference_model`	a Bayesian phylogenetic inference model, as returned by create_inference_model
`beast2_options`	'BEAST2' options, as can be created by create_beast2_options

Value

a list with the following elements:

- `estimates`: a data frame with 'BEAST2' parameter estimates
- `[alignment_id]_trees`: a `multiPhylo` containing the phylogenies in the 'BEAST2' posterior. `[alignment_id]` is the ID of the alignment. For example, when running `bbt_run_from_model` with `anthus_aco.fas`, this element will have name `anthus_aco_trees`
- `operators`: a data frame with the 'BEAST2' MCMC operator acceptances
- `output`: a numeric vector with the output sent to standard output and error streams
- `ns`: (optional) the results of a marginal likelihood estimation, will exist only when `create_ns_mcmc` was used for `mcmc`. This structure will contain the following elements:
  - `marg_log_lik` the marginal log likelihood estimate
  - `marg_log_lik_sd` the standard deviation around the estimate
  - `estimates` the parameter estimates created during the marginal likelihood estimation
  - `trees` the trees created during the marginal likelihood estimation

Author(s)

Richèl J.C. Bilderbeek

See Also

Use `remove_burn_ins` to remove the burn-ins from the posterior's estimates (`posterior$estimates`)

Examples

```
if (beautier::is_on_ci() && is_beast2_installed()) {
  beastier::remove_beaustier_folders()
  beastier::check_empty_beaustier_folders()

  # Simple short inference
```

```
  inference_model <- create_test_inference_model()

  # Default BEAST2 options
  beast2_options <- create_beast2_options()

  bbt_run_from_model(
    fasta_filename = get_babette_path("anthus_aco.fas"),
    inference_model = inference_model,
    beast2_options = beast2_options
  )

  # Cleanup
  bbt_delete_temp_files(
    inference_model = inference_model,
    beast2_options = beast2_options
  )
  beastier::remove_beaustier_folders()
  beastier::check_empty_beaustier_folders()
}
```

`bbt_self_test` *Do a self test to verify babette that works correctly.*

Description

Do a self test to verify babette that works correctly.

Usage

```
bbt_self_test(beast2_options = beastier::create_beast2_options())
```

Arguments

`beast2_options`	'BEAST2' options, as can be created by create_beast2_options

Value

Nothing. Will raise an exception if something is wrong.

Author(s)

Richèl J.C. Bilderbeek

Examples

```
if (beautier::is_on_ci() && is_beast2_installed()) {
  beastier::remove_beaustier_folders()
  beastier::check_empty_beaustier_folders()

  bbt_self_test()
```

```
  beastier::remove_beaustier_folders()
  beastier::check_empty_beaustier_folders()
}
```

`check_beast2_pkgs` *Checks if* `bbt_run` *has the 'BEAST2' packages needed to process its arguments. Will stop if not.*

Description

For example, to use a Nested Sampling MCMC, the 'BEAST2' 'NS' package needs to be installed.

Usage

```
check_beast2_pkgs(mcmc, beast2_path = get_default_beast2_bin_path())
```

Arguments

`mcmc`	the MCMC options, see create_mcmc
`beast2_path`	name of either a 'BEAST2' binary file (usually simply `beast`) or a 'BEAST2' jar file (usually has a `.jar` extension). Use `get_default_beast2_bin_path` to get the default BEAST binary file's path Use `get_default_beast2_jar_path` to get the default BEAST jar file's path

Value

Nothing.

Examples

```
if (beautier::is_on_ci() && is_beast2_installed()) {
  beastier::remove_beaustier_folders()
  beastier::check_empty_beaustier_folders()

  # Minimal BEAST2 setup
  check_beast2_pkgs(mcmc = create_mcmc())

  # BEAST2 with NS package installed
  if (is_beast2_ns_pkg_installed()) {
    check_beast2_pkgs(mcmc = create_ns_mcmc())
  }

  beastier::remove_beaustier_folders()
  beastier::check_empty_beaustier_folders()
}
```

create_test_bbt_run_output *Get an example output of* bbt_run *or* bbt_run_from_model.

Description

This output is used in testing.

Usage

```
create_test_bbt_run_output()
```

Value

the same results as bbt_run or bbt_run_from_model

Author(s)

Richèl J.C. Bilderbeek

Examples

```
beastier::remove_beaustier_folders()
beastier::check_empty_beaustier_folders()

create_test_bbt_run_output()

beastier::remove_beaustier_folders()
beastier::check_empty_beaustier_folders()
```

create_test_ns_output *Create NS testing output*

Description

Create testing output similar to when running a 'BEAST2' run with nested sampling

Usage

```
create_test_ns_output()
```

Value

a text of type character vector.

Author(s)

Richèl J.C. Bilderbeek

See Also

Use parse_beast2_output_to_ns to parse this output to a Nested Sampling result. See create_ns_mcmc to see how to do a marginal likelihood estimation using Nested Sampling.

Examples

```
beastier::remove_beaustier_folders()
beastier::check_empty_beaustier_folders()

create_test_ns_output()

beastier::remove_beaustier_folders()
beastier::check_empty_beaustier_folders()
```

`default_params_doc` *This function does nothing. It is intended to inherit is parameters' documentation.*

Description

This function does nothing. It is intended to inherit is parameters' documentation.

Usage

```
default_params_doc(
  beast2_input_filename,
  beast2_options,
  beast2_output_log_filename,
  beast2_output_state_filename,
  beast2_output_trees_filenames,
  beast2_path,
  beast2_working_dir,
  cleanup,
  clock_model,
  clock_models,
  fasta_filename,
  fasta_filenames,
  inference_model,
  mcmc,
  mrca_prior,
  mrca_priors,
  overwrite,
  rng_seed,
```

```
  site_model,
  site_models,
  tipdates_filename,
  tree_prior,
  tree_priors,
  verbose
)
```

Arguments

beast2_input_filename	path of the 'BEAST2' configuration file. By default, this file is put in a temporary folder with a random filename, as the user needs not read it: it is used as input of 'BEAST2'. Specifying a beast2_input_filename allows to store that file in a more permanently stored location.
beast2_options	'BEAST2' options, as can be created by create_beast2_options
beast2_output_log_filename	name of the log file created by 'BEAST2', containing the parameter estimates in time. By default, this file is put a temporary folder with a random filename, as the user needs not read it: its content is parsed and returned by this function. Specifying a beast2_output_log_filename allows to store that file in a more permanently stored location.
beast2_output_state_filename	name of the final state file created by 'BEAST2', containing the operator acceptances. By default, this file is put a temporary folder with a random filename, as the user needs not read it: its content is parsed and returned by this function. Specifying a beast2_output_state_filename allows to store that file in a more permanently stored location.
beast2_output_trees_filenames	name of the one or more trees files created by 'BEAST2', one per alignment. By default, these files are put a temporary folder with a random filename, as the user needs not read it: their content is parsed and returned by this function. Specifying beast2_output_trees_filenames allows to store these one or more files in a more permanently stored location.
beast2_path	name of either a 'BEAST2' binary file (usually simply beast) or a 'BEAST2' jar file (usually has a .jar extension). Use get_default_beast2_bin_path to get the default BEAST binary file's path Use get_default_beast2_jar_path to get the default BEAST jar file's path
beast2_working_dir	the folder 'BEAST2' will work in. This is an (empty) temporary folder by default. This allows to call 'BEAST2' in multiple parallel processes, as each process can have its own working directory
cleanup	set to FALSE to keep all temporary files
clock_model	one clock model, see create_clock_model
clock_models	one or more clock models, see create_clock_models
fasta_filename	a FASTA filename

`fasta_filenames`
: one or more FASTA filename, each with one alignment

`inference_model`
: a Bayesian phylogenetic inference model, as returned by create_inference_model

`mcmc`
: the MCMC options, see create_mcmc

`mrca_prior`
: one Most Recent Common Ancestor prior, as returned by `create_mrca_prior`

`mrca_priors`
: a list of one or more Most Recent Common Ancestor priors, as returned by `create_mrca_prior`

`overwrite`
: will 'BEAST2' overwrite files? Like 'BEAST2', this is set to TRUE by default. If TRUE, 'BEAST2' will overwrite the `beast2_options$output_state_filename` if its present. If FALSE, 'BEAST2' will not overwrite the `beast2_options$output_state_filename` if its present and babette will give an error message. Note that if `overwrite` is set to FALSE when a `tracelog` (see create_tracelog), `screenlog` (see create_screenlog) or `treelog` (see create_treelog) file already exists, 'BEAST2' (and thus babette) will freeze.

`rng_seed`
: the random number generator seed. Must be either `NA` or a positive non-zero value. An RNG seed of `NA` results in 'BEAST2' picking a random seed.

`site_model`
: one site model, see create_site_models

`site_models`
: one or more site models, see create_site_models

`tipdates_filename`
: name of the file containing tip dates

`tree_prior`
: one tree priors, as created by create_tree_prior

`tree_priors`
: one or more tree priors, see create_tree_priors

`verbose`
: set to TRUE for more output

Note

This is an internal function, so it should be marked with `@noRd`. This is not done, as this will disallow all functions to find the documentation parameters

Author(s)

Richèl J.C. Bilderbeek

`get_alignment_ids_from_xml` *Get the alignment IDs from one or more 'BEAST2' XML input files.*

Description

Get the alignment IDs from one or more 'BEAST2' XML input files.

Usage

```
get_alignment_ids_from_xml(xml_filename)
```

Arguments

xml_filename	name of a 'BEAST2' XML input file.

Value

a character vector with one or more alignment IDs.

Author(s)

Richèl J.C. Bilderbeek

Examples

```
beastier::remove_beaustier_folders()
beastier::check_empty_beaustier_folders()

alignment_ids <- get_alignment_ids_from_xml(
  get_babette_path("anthus_2_4.xml")
)

beastier::remove_beaustier_folders()
beastier::check_empty_beaustier_folders()
```

---

get_babette_path *Get the full path of a file in the* inst/extdata *folder*

Description

Get the full path of a file in the inst/extdata folder

Usage

```
get_babette_path(filename)
```

Arguments

filename	the file's name, without the path

Value

the full path of the filename, if and only if the file is present. Will stop otherwise.

Author(s)

Richèl J.C. Bilderbeek

See Also

for more files, use get_babette_paths

Examples

```
beastier::remove_beaustier_folders()
beastier::check_empty_beaustier_folders()

get_babette_path("anthus_aco.fas")

beastier::remove_beaustier_folders()
beastier::check_empty_beaustier_folders()
```

`get_babette_paths` *Get the full paths of files in the* `inst/extdata` *folder*

Description

Get the full paths of files in the `inst/extdata` folder

Usage

```
get_babette_paths(filenames)
```

Arguments

`filenames`	the files' names, without the path

Value

the filenames' full paths, if and only if all files are present. Will stop otherwise.

Author(s)

Richèl J.C. Bilderbeek

See Also

for one file, use `get_babette_path`

Examples

```
beastier::remove_beaustier_folders()
beastier::check_empty_beaustier_folders()

get_babette_paths(c("anthus_aco.fas", "anthus_nd2.fas"))

beastier::remove_beaustier_folders()
beastier::check_empty_beaustier_folders()
```

`parse_beast2_output` *Process the 'BEAST2' output dependent on 'BEAST2' package specifics*

Description

Process the 'BEAST2' output dependent on 'BEAST2' package specifics

Usage

```
parse_beast2_output(out, inference_model)
```

Arguments

`out`	a list with the complete babette output, with elements: • `output` textual output of a 'BEAST2' run
`inference_model`	a Bayesian phylogenetic inference model, as returned by create_inference_model

Value

complete babette output with added attributes, which depends on the 'BEAST2' package.

- `marg_log_lik` the marginal log likelihood estimate
- `marg_log_lik_sd` the standard deviation around the estimate
- `estimates` the parameter estimates created during the marginal likelihood estimation
- `trees` the trees created during the marginal likelihood estimation

Author(s)

Richèl J.C. Bilderbeek

`parse_beast2_output_to_ns` *Parse BEAST2 NS output*

Description

Parse the BEAST2 output when run with the BEAST2 NS ('Nested Sampling') package.

Usage

```
parse_beast2_output_to_ns(output)
```

Arguments

output	screen output

Value

a list with the following elements:

- marg_log_lik the marginal log likelihood estimate
- marg_log_lik_sd the standard deviation around the estimate

Author(s)

Richèl J.C. Bilderbeek

See Also

use create_test_ns_output to obtain a test screen output.

Examples

```
beastier::remove_beaustier_folders()
beastier::check_empty_beaustier_folders()

parse_beast2_output_to_ns(
  output = create_test_ns_output()
)

beastier::remove_beaustier_folders()
beastier::check_empty_beaustier_folders()
```

---

plot_densitree *Draw multiple trees on top of one another.*

Description

Draw multiple trees on top of one another.

Usage

```
plot_densitree(phylos, ...)
```

Arguments

phylos	one or more phylogenies, must be of class multiPhylo
...	options to be passed to phangorn's densiTree function

Value

nothing. Will produce a plot.

Author(s)

Richèl J.C. Bilderbeek

Examples

```
if (beautier::is_on_ci() && is_beast2_installed()) {
  beastier::remove_beaustier_folders()
  beastier::check_empty_beaustier_folders()

  inference_model <- create_test_inference_model()
  beast2_options <- create_beast2_options()

   out <- bbt_run_from_model(
    get_babette_path("anthus_aco.fas"),
    inference_model = inference_model,
    beast2_options = beast2_options
  )
  bbt_delete_temp_files(
    inference_model = inference_model,
    beast2_options = beast2_options
  )

  plot_densitree(out$anthus_aco_trees)

  # Clean up temporary files created by babette
  bbt_delete_temp_files(
    inference_model = inference_model,
    beast2_options = beast2_options
  )
  beastier::remove_beaustier_folders()
  beastier::check_empty_beaustier_folders()
}
```

---

prepare_file_creation *Internal function to prepare for 'BEAST2' creating files*

Description

The inference model and 'BEAST2' options contain paths that may point to sub-sub-sub folders. Create those folders and test if these folders can be written to

Usage

```
prepare_file_creation(inference_model, beast2_options)
```

Arguments

inference_model	a Bayesian phylogenetic inference model, as returned by create_inference_model
beast2_options	'BEAST2' options, as can be created by create_beast2_options

Value

Nothing.

Examples

```
# This example will fail on the CRAN
# r-oldrel-macos-x86_64 platform
if (rappdirs::app_dir()$os != "mac") {
  beastier::remove_beaustier_folders()
  beastier::check_empty_beaustier_folders()

  # For a test inference model, the files can be prepared
  inference_model <- create_test_inference_model()
  beast2_options <- create_beast2_options()
  prepare_file_creation(inference_model, beast2_options)

  beastier::remove_beaustier_folders()
  beastier::check_empty_beaustier_folders()
}
```

---

update_babette *Deprecated function.*

Description

Update all babette dependencies, by installing their latest versions.

Usage

```
update_babette(upgrade = "default")
```

Arguments

upgrade	Deprecated.

Details

See https://github.com/richelbilderbeek/babetteinstall how to do this.

Value

Nothing.

Author(s)

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